

```

      11      20      29      38      47      56
5' ACG NGA ATG GCC TTC CCG CGC CCC AAG AAG AAC CTG CCC CAG CCC AAG NAG GCT
      M  A  F  P  R  P  K  K  N  L  P  Q  P  K  X  A

      65      74      83      92      101      110
GCC ACA GAG GGC CCC AGT GCT GCC TCT GGT GTG CCC CAG ACG GGA CCT GGC AGG
A  T  E  G  P  S  A  A  S  G  V  P  Q  T  G  P  G  R

      119      128      137      146      155      164
GAG GTG GCA GCC ACC CGG CCC AAG ACC ACC AAG TCG GGG AAG GCG CTG GCC AAG
E  V  A  A  T  R  P  K  T  T  K  S  G  K  A  L  A  K

      173      182      191      200      209      218
ACT CGG TGG GTG GAG CCT CAG AAT GTT GTG GCA GCA GCT GCT GCC AAG GCC AAG
T  R  W  V  E  P  Q  N  V  V  A  A  A  A  A  K  A  K

      227      236      245      254      263      272
ATG GCC ACG AGC ATC CCT GAG CCG GAG GGT GCA GCT GCT GCC ACT GCT CAG CAC
M  A  T  S  I  P  E  P  E  G  A  A  A  A  T  A  Q  H

      281      290      299      308      317      326
AGT GCT GAG CCC TGG GCC AGG ATG GGA GGC AAG AGG ACC AAG AAG TCC AAG CAC
S  A  E  P  W  A  R  M  G  G  K  R  T  K  K  S  K  H

      335      344      353      362      371      380
CTG GAT GAT GAG TAT GAG AGC AGC GAG GAG GAG AGA GAG ACT CCC GCG GTC CCA
L  D  D  E  Y  E  S  S  E  E  E  R  E  T  P  A  V  P

      389      398      407      416      425      434
CCC ACC TGG AGA GCA TCA CAG CCC TCA TTG ACG GTG CGG GCT CAG TTG GCC CCT
P  T  W  R  A  S  Q  P  S  L  T  V  R  A  Q  L  A  P

      443      452      461      470      479      488
CGG CCC CCG ATG GCC CCG AGG TCC CAG ATA CCC TCA AGG CAC GTA CTG TGC CTG
R  P  P  M  A  P  R  S  Q  I  P  S  R  H  V  L  C  L

      497      506      515      524      533      542
CCC CCC CGC AAC GTG ACC CTT CTG CAG GAG AGG GCA AAT AAG TTG GTG AAA TAC
P  P  R  N  V  T  L  L  Q  E  R  A  N  K  L  V  K  Y

      551      560      569      578      587      596
CTG ATG ATT AAG GAC TAC AAG AAG ATC CCC ATC AAG CGC GCA GAC ATG CTG AAG
L  M  I  K  D  Y  K  K  I  P  I  K  R  A  D  M  L  K

```

FIGURE 1A

```

        605          614          623          632          641          650
GAT GTC ATC AGA GAA TAT GAT GAA CAT TTC CCT GAG ATC ATT GAA CGA GCA ACG
D  V  I  R  E  Y  D  E  H  F  P  E  I  I  E  R  A  T

        659          668          677          686          695          704
TAC ACC CTG GAA AAG AAG TTT GGG ATC CAC CTG AAG GAG ATC GAC AAG GAA GAA
Y  T  L  E  K  K  F  G  I  H  L  K  E  I  D  K  E  E

        713          722          731          740          749          758
CAC CTG TAT ATT CTT GTC TGC ACA CGG GAC TCC TCA GCT CGC CTC CTT GGA AAA
H  L  Y  I  L  V  C  T  R  D  S  S  A  R  L  L  G  K

        767          776          785          794          803          812
ACC AAG GAC ACT CCC AGG CTG AGT CTC CTC TTG GTG ATT CTG GGC GTC ATC TTC
T  K  D  T  P  R  L  S  L  L  L  V  I  L  G  V  I  F

        821          830          839          848          857          866
ATG AAT GGC AAC CGT GCC AGC GAG GCT GTC CTC TGG GAG GCA CTA CGC AAG ATG
M  N  G  N  R  A  S  E  A  V  L  W  E  A  L  R  K  M

        875          884          893          902          911          920
GGA CTG CGT CCT GGG GTG AGA CAT CCC CTC CTT GGA GAT CTA AGG AAA CTT CTC
G  L  R  P  G  V  R  H  P  L  L  G  D  L  R  K  L  L

        929          938          947          956          965          974
ACC TAT GAG TTT GTA AAG CAG AAA TAC CTG GAC TAC AGA CGA GTG CCC AAC AGC
T  Y  E  F  V  K  Q  K  Y  L  D  Y  R  R  V  P  N  S

        983          992          1001          1010          1019          1028
AAC CCC CCG GAG TAT GAG TTC CTC TGG GGC CTC CGT TCC TAC CAT GAG ACT AGC
N  P  P  E  Y  E  F  L  W  G  L  R  S  Y  H  E  T  S

        1037          1046          1055          1064          1073          1082
AAG ATG AAA GTG CTG AGA TTC ATT GCA GAG GTT CAG AAA AGA GAC CCT CGT GAC
K  M  K  V  L  R  F  I  A  E  V  Q  K  R  D  P  R  D

        1091          1100          1109          1118          1127          1136
TGG ACT GCA CAG TTC ATG GAG GCT GCA GAT GAG GCC TTG GAT GCT CTG GAT GCT
W  T  A  Q  F  M  E  A  A  D  E  A  L  D  A  L  D  A

        1145          1154          1163          1172          1181          1190
GCT GCA GCT GAG GCC GAA GCC CGG GCT GAA GCA AGA ACC CGC ATG GGA ATT GGA
A  A  A  E  A  E  A  R  A  E  A  R  T  R  M  G  I  G

        1199          1208          1217          1226          1235          1244
GAT GAG GCT GTG TCT GGG CCC GGA GCT GGG ATG ACA TTG AGT TTG AGC TGC TGA
D  E  A  V  S  G  P  G  A  G  M  T  L  S  L  S  C

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CCT 3'

FIGURE 1B

FIGURE 2A

268	F	M	N	G	N	R	A	S	E	A	V	L	W	E	A	L	R	K	M	G	L	R	P	G	V	R	H	P	L	L	SEQ ID NO-1
209	F	L	K	G	N	S	A	T	E	E	E	I	W	K	F	M	N	V	L	G	A	Y	D	G	E	E	H	L	I	Y	GI 608993
235	F	I	E	G	Y	C	T	P	E	E	V	I	W	E	A	L	N	M	M	G	L	Y	D	G	M	E	H	L	I	Y	GI 533511
253	F	M	K	G	N	R	A	T	E	Q	E	V	W	Q	F	L	H	G	V	G	V	Y	A	G	K	K	H	L	I	F	GI 1165170
203	Y	V	K	G	R	G	A	R	E	G	A	V	W	N	V	L	R	I	L	G	L	R	P	W	K	K	H	S	T	F	GI 1040691
298	G	D	L	R	K	L	L	T	Y	E	F	V	K	Q	K	Y	L	D	Y	R	R	V	P	N	S	N	P	P	E	Y	SEQ ID NO-1
239	G	E	P	R	K	F	I	T	Q	D	L	V	Q	E	K	Y	L	K	Y	E	Q	V	P	N	S	D	P	P	R	Y	GI 608993
265	G	E	P	R	K	L	L	T	Q	D	W	V	Q	E	N	Y	L	E	Y	R	Q	V	P	G	S	D	P	A	R	Y	GI 533511
283	G	E	P	E	E	F	I	-	R	D	V	V	R	E	N	Y	L	E	Y	R	Q	V	P	G	S	D	P	P	S	Y	GI 1165170
233	G	D	V	R	K	I	I	T	E	E	F	V	Q	Q	N	Y	L	K	Y	Q	R	V	P	H	I	E	P	P	E	Y	GI 1040691
328	E	F	L	W	G	L	R	S	Y	H	E	T	S	K	M	K	V	L	R	F	I	A	E	V	Q	K	R	D	P	R	SEQ ID NO-1
269	Q	F	L	W	G	P	R	A	Y	A	E	T	T	K	M	K	V	L	E	F	L	A	K	M	N	G	A	T	P	R	GI 608993
295	E	F	L	W	G	P	R	A	H	A	E	I	R	K	M	S	L	L	K	F	L	A	K	V	N	G	S	D	P	R	GI 533511
312	E	F	L	W	G	P	R	A	H	A	E	T	T	K	M	K	V	L	E	V	L	A	K	V	N	G	T	V	P	S	GI 1165170
263	E	F	F	W	G	S	R	A	N	R	E	I	T	K	M	Q	I	M	E	F	L	A	R	V	F	K	K	D	P	Q	GI 1040691
358	D	W	T	A	Q	F	M	E	A	A	D	E	A	L	D	A	L	D	A	A	A	A	E	A	E	A	R	A	E	A	SEQ ID NO-1
299	D	F	P	S	H	Y	E	E	-	-	-	-	-	-	-	A	L	R	D	E	E	E	R	A	Q	V	R	S	S	V	GI 608993
325	S	F	P	L	W	Y	E	E	-	-	-	-	-	-	-	A	L	K	D	E	E	E	R	A	Q	D	R	I	A	T	GI 533511
342	A	F	P	N	L	Y	Q	L	-	-	-	-	-	-	-	A	L	R	D	Q	A	-	-	-	-	-	-	G	G	GI 1165170	
293	A	W	P	S	R	Y	R	E	A	L	E	Q	A	-	R	A	L	R	E	A	N	L	A	A	O	A	P	-	-	-	GI 1040691
388	R	T	R	M	G	I	G	D	E	A	V	S	G	P	G	A	G	M	T	L	S	L	S	C						SEQ ID NO-1	
322	R	A	R	R	R	T	T	A	T	T	F	R	A	R	S	R	A	-	P	F	S	R	S	S	H	P	M			GI 608993	
348	T	D	D	T	T	A	M	A	S	A	-	S	S	S	A	T	G	-	S	F	S	-	-	-	Y	P	E			GI 533511	
358	V	P	R	R	R	V	Q	G	K	G	V	H	S	K	A	P	-	-	-	-	S	Q	K	S	S	N	M			GI 1165170	
319	-	-	R	S	S	V	S	E	D																				GI 1040691		

FIGURE 2B

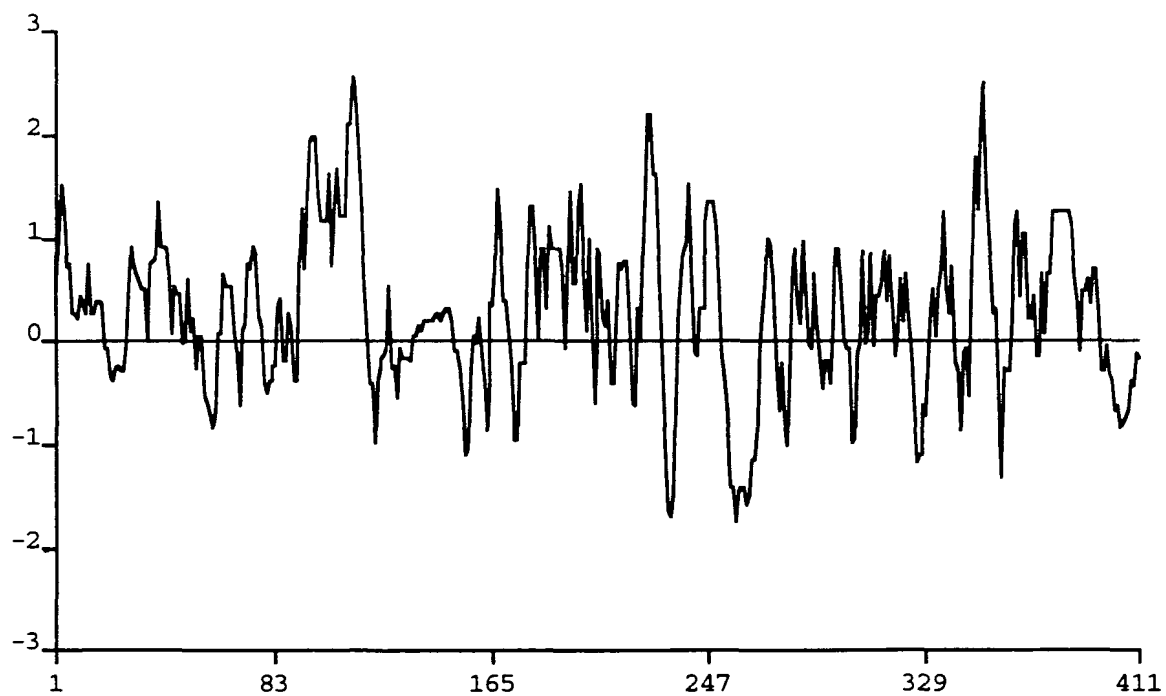


FIGURE 3

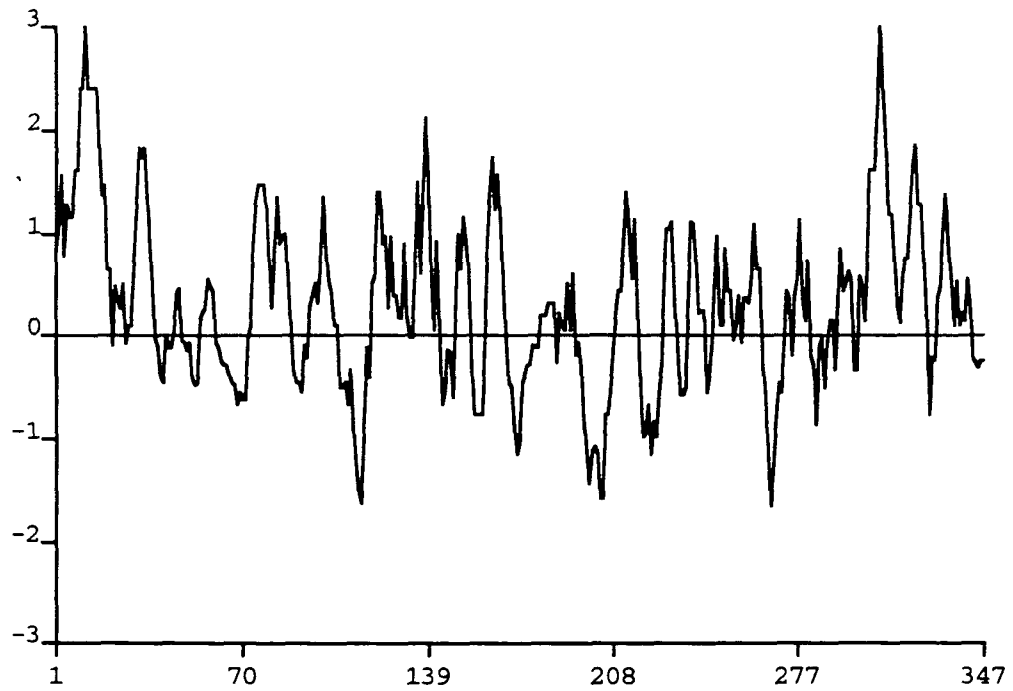


FIGURE 4